

1 GCGGGCGCGG AGGAGGTGGT GCTGCAGCCC ATCAAGGAGA TCTCCGGCGT
 5 51 CGTGAAGCTG CCGGGGTCCA AGTCGCTCTC CAACCGGATC CTCCTGCTCT
 101 CCGCCCTCGC CGAGGGAACA ACTGTGGTGG ATAACCTTTT AAACAGTGAG
 15 151 GACGTCCACT ACATGCTCGG GGCCCTGAAA ACCCTCGGAC TCTCTGTGGA
 201 AGCGGACAAA GCTGCCAAAA GAGCGGTAGT TGTGCTGTGT GGTGGCAAGT
 251 TCCCAGTTGA GAAGGATGCG AAAGAGGAGG TGCAGCTCTT CTTGGGGAAT
 15 301 GCTGGAACTG CAATGCGATC ATTGACAGCA GCCGTAAC TG CTGCTGGAGG
 351 AAATGCAACT TATGTGCTTG ATGGAGTGCC AAGAATGCGG GAGAGACCCA
 401 TTGGCGACTT GGTGTCGGA TTGAAACAGC TTGGTGCGGA TGTGATTGT
 20 451 TTCCTTGGCA CTGACTGCCC ACCTGTTTCGT GTCAAGGGAA TCGGAGGGCT
 501 ACCTGGTGGC AAGGTTAAGT TATCTGGTTC CATCAGCAGT CAGTACTTGA
 25 551 GTGCCTTGCT GATGGCTGCT CCTTTAGCTC TTGGGGATGT GGAGATTGAA
 601 ATCATTGATA AACTGATCTC CATCCCTTAT GTTGAAATGA CATTGAGATT
 651 GATGGAGCGT TTTGGCGTGA AAGCAGAGCA TTCTGATAGC TGGGACAGAT
 30 701 TCTACATCAA GGGAGGTCAA AAATACAAGT CCCCTAAAAA TGCCTACGTG
 751 GAAGGTGATG CCTCAAGTGC GAGCTATTTT TTGGCTGGTG CTGCAATCAC
 35 801 TGGAGGGACT GTGACTGTTG AAGGTTGTGG CACCACCAGT CTGCAGGGTG
 851 ATGTGAAATT TGCCGAGGTA CTCGAGATGA TGGGAGCGAA GGTACATGG
 901 ACTGAAACTA GCGTAACTGT TACCGGTCCA CAACGTGAGC CATTTGGGAG
 40 951 GAAACACCTA AAAGCTATTG ATGTTAACAT GAACAAAATG CCCGATGTCG
 1001 CCATGACTCT TGCCGTGGTT GCCCTATTTG CTGATGGCCC AACTGCTATC
 45 1051 AGAGATGTGG CTTCTGGAG AGTAAAGGAG ACCGAGAGGA TGGTTGCAAT
 1101 CCGGACTGAG CTAACAAAGC TGGGAGCGTC GGTCGAGGAA GGACTGGACT
 1151 ACTGCATTAT CACACGCCC GAGAAGCTGA ACGTAACGGC CATCGACACC
 50 1201 TACGATGACC ACAGGATGGC CATGGCCTTC TCCCTCGCCG CCTGCGCCGA
 1251 CGTGCCCTGTG ACCATCCGGG ACCCCGGCTG CACCCGCAAG ACCTTCCCAG
 55 1301 ACTACTTCGA CGTGCTGAGC ACTTTCGTCA AGAACTAA

Figure 1.

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1  AGAEEVVLQP IKEISGVVKL PGSKSLSNRI LLSALAEGT TVVDNLLNSE
51 DVHYMLGALK TLGLSVEADK AAKRAVVVGC GGKFPVEKDA KEEVQLFLGN
101 AGTAMRSLTA AVTAAGGNAT YVLDGVPRMR ERPIGDLVVG LKQLGADVDC
151 FLGTDCPPVR VKGIGGLPGG KVKLSGSISS QYLSALLMAA PLALGDVEIE
201 IIDKLISIPY VEMTLRLMER FGVKAEHSDS WDRFYIKGGQ KYKSPKNAYV
251 EGDASSASYF LAGAAITGGT VTVEGCGTTS LQGDVKFAEV LEMMGAKVTW
301 TETSVTVTGP QREPFGRKHL KAIDVNMNMK PDVAMTLAVV ALFADGPTAI
351 RDVASWRVKE TERMVAIRTE LTKLGASVEE GLDYCIITPP EKLNVTAIDT
401 YDDHRMAMAF SLAACADVPV TIRDPGCTRK TFPDYFDVLS TFVKN*

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Figure 2

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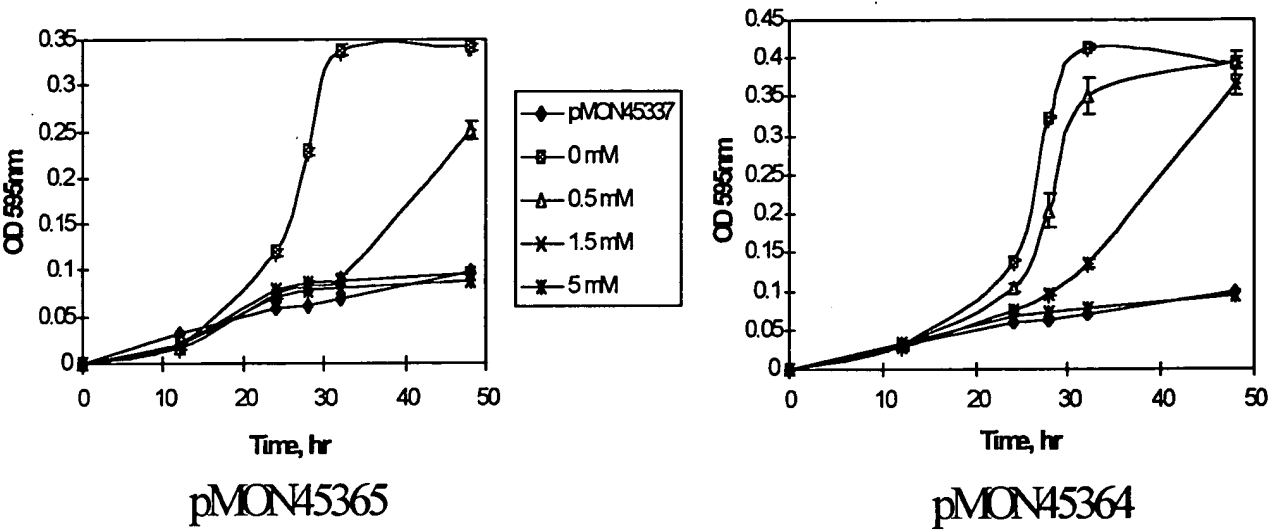
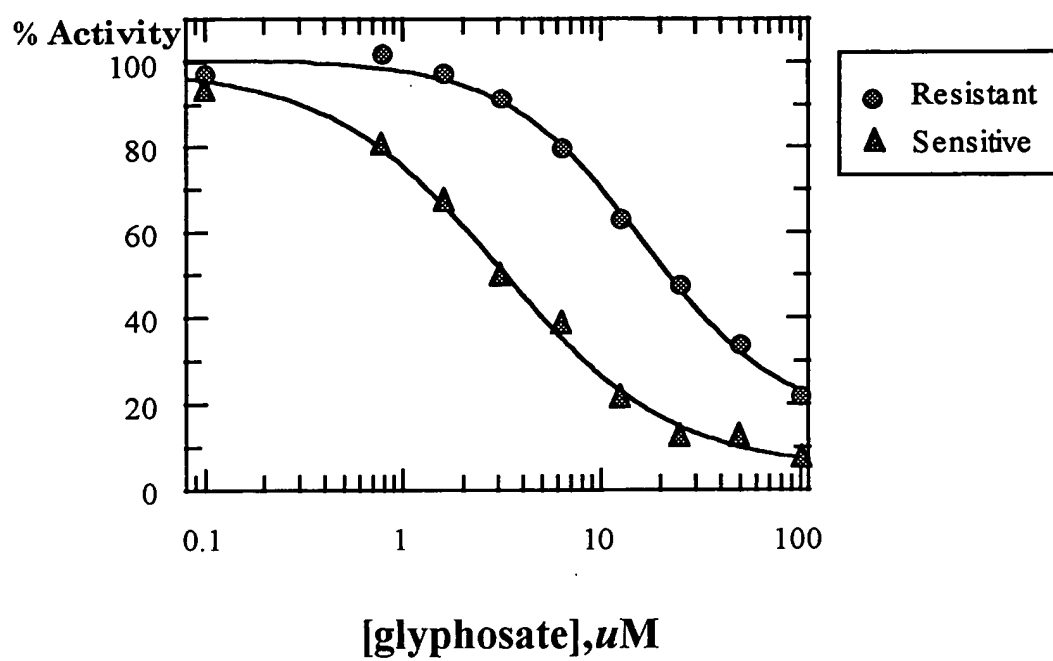


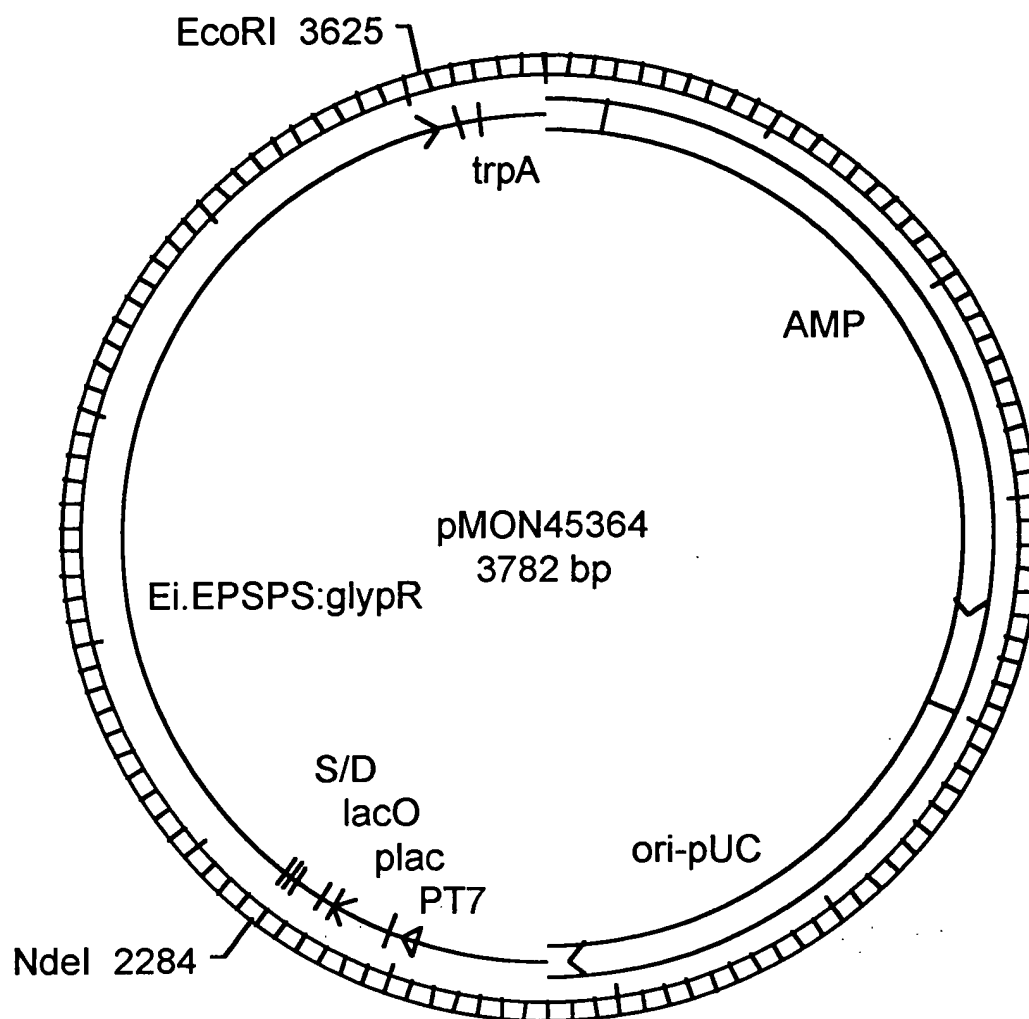
Figure 3

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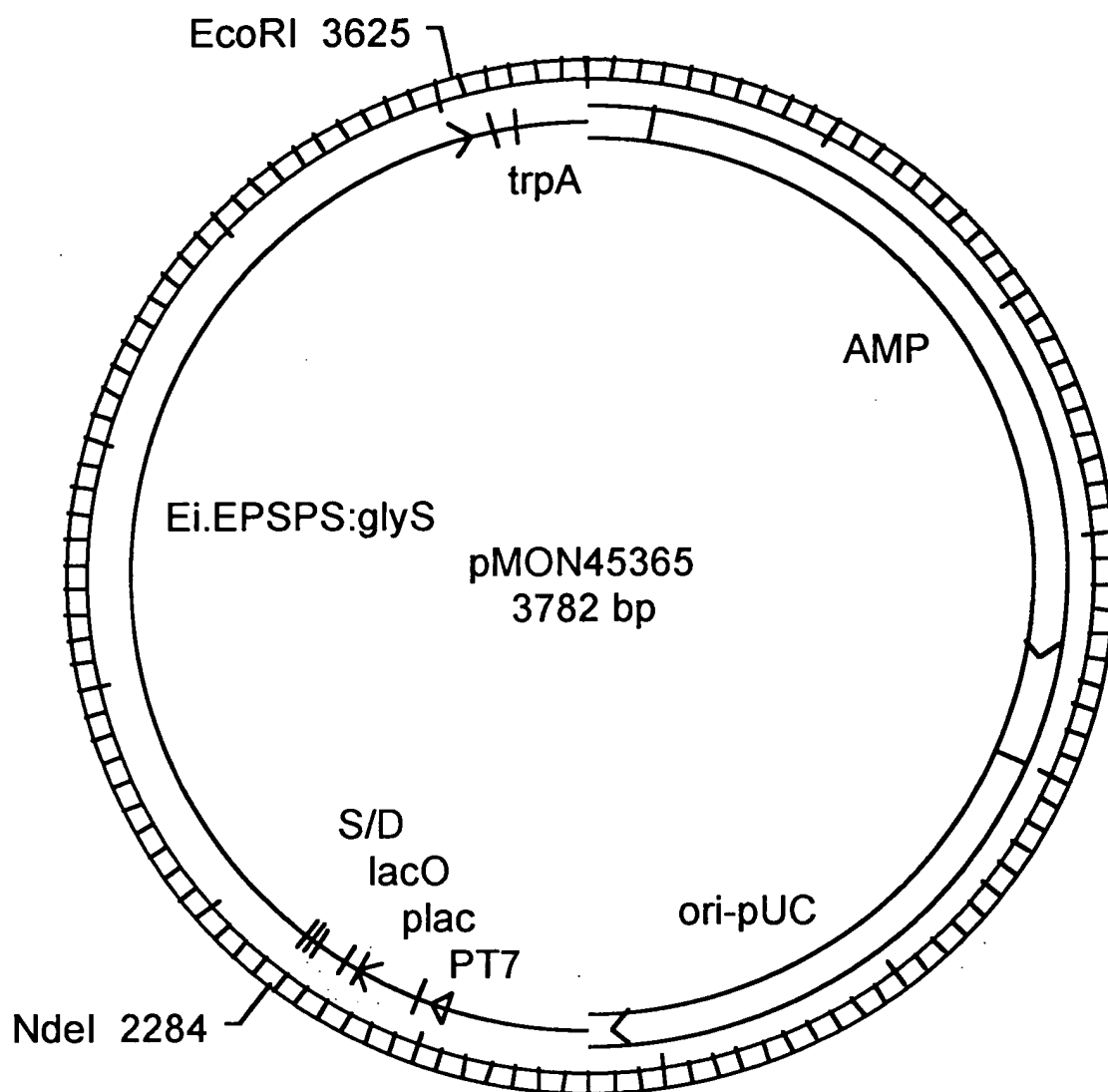
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**Figure 4**



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Figure 5



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Figure 6

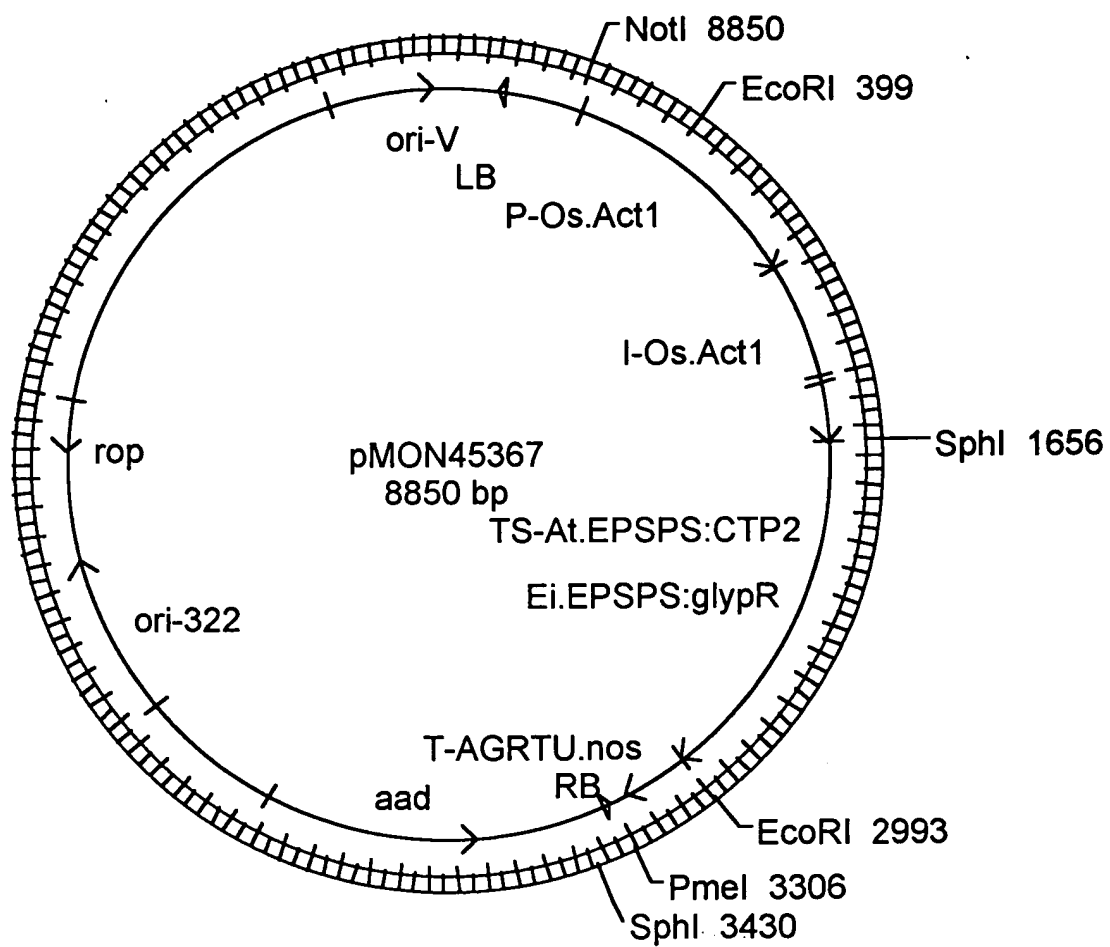
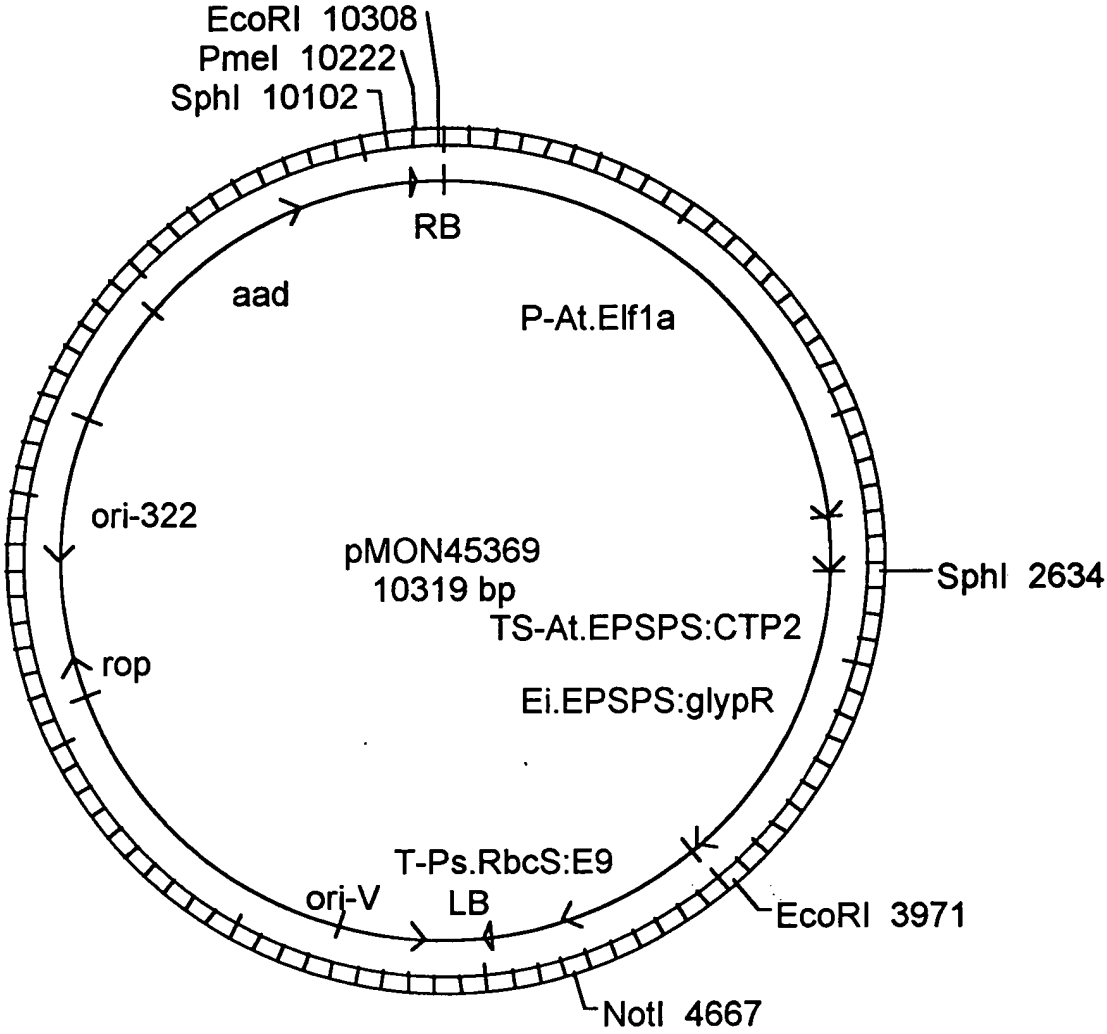


Figure 7



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Figure 8

Figure 9

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      .       .       .       .       .
1  AGAEEVVLQPIKEISGVVKLPGSKSLSNRILLLSALAEGTTVVDNLLNSE 50
      |||
5  1  AGAEEVVLQPIKEISGVVKLPGSKSLSNRILLLSALAEGTTVVDNLLNSE 50
      .       .       .       .       .
51 DVHYMLGALKTLGLSVEADKAAKRAVVVGCGGKFPVEKDAKEEVQLFLGN 100
      |||
10 51 DVHYMLGALKTLGLSVEADKAAKRAVVVGCGGKFPVEKDAKEEVQLFLGN 100
      .       .       .       .       .
101 AGTAMRSLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDC 150
      |||
101 AGTAMRPLTAAVTAAGGNATYVLDGVPRMRERPIGDLVVGLKQLGADVDC 150
      .       .       .       .       .
15 151 FLGTDCPPVRVKGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIE 200
      |||
151 FLGTDCPPVRVKGIGGLPGGKVKLSGSISSQYLSALLMAAPLALGDVEIE 200
      .       .       .       .       .
20 201 IIDKLISIPYVENTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
      |||
201 IIDKLISIPYVENTLRLMERFGVKAHSDSWDRFYIKGGQKYKSPKNAYV 250
      .       .       .       .       .
25 251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
      |||
251 EGDASSASYFLAGAAITGGTVTVEGCGTTSLQGDVKFAEVLEMMGAKVTW 300
      .       .       .       .       .
301 TETSVTVTGPQREPFGRKHLKAIDVNMNKMPDVAMTLAVVALFADGPTAI 350
      |||
301 TETSVTVTGPQREPFGRKHLKAIDVNMNKMPDVAMTLAVVALFADGPTAI 350

```

351 RDVASWRVKETERMVAIRTELTKLGASVEEGLDYCIITPPEKLNVT AIDT 400

|||||

351 RDVASWRVKETERMVAIRTELTKLGASVEEGPDYCIITPPEKLNVT AIDT 400

5

401 YDDHRMAMAFSLAACADVPVTIRDPGCTRKTFPDYFDVLSTFVKN* 445

|||||

401 YDDHRMAMAFSLAACADVPVTIRDPGCTRKTFPDYFDVLSTFVKN* 445

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Figure 9 (cont)

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